

2/15 0300

#2



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## RAW SEQUENCE LISTING

DATE: 01/29/2002

PATENT APPLICATION: US/09/998,966

TIME: 15:45:55

Input Set : N:\Crf3\RULE60\09998966.txt

Output Set: N:\CRF3\01292002\I998966.raw

3 <110> APPLICANT: Shimkets, Richard  
 4 Fernandes, Elma  
 5 Boldog, Ferenc  
 7 <120> TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY  
 9 <130> FILE REFERENCE: 15966-551  
 11 <140> CURRENT APPLICATION NUMBER: 09/998,966  
 12 <141> CURRENT FILING DATE: 2001-10-31  
 14 <150> PRIOR APPLICATION NUMBER: 09/569,269  
 15 <151> PRIOR FILING DATE: 2000-05-11  
 17 <150> PRIOR APPLICATION NUMBER: 60/134,315  
 18 <151> PRIOR FILING DATE: 1999-05-14  
 20 <150> PRIOR APPLICATION NUMBER: 60/175,744  
 21 <151> PRIOR FILING DATE: 2000-01-12  
 23 <150> PRIOR APPLICATION NUMBER: 60/188,274  
 24 <151> PRIOR FILING DATE: 2000-03-10  
 26 <160> NUMBER OF SEQ ID NOS: 52  
 28 <170> SOFTWARE: PatentIn Ver. 2.0  
 30 <210> SEQ ID NO: 1  
 31 <211> LENGTH: 670  
 32 <212> TYPE: DNA  
 33 <213> ORGANISM: Homo sapiens  
 35 <220> FEATURE:  
 36 <221> NAME/KEY: CDS  
 37 <222> LOCATION: (130)..(639)  
 39 <400> SEQUENCE: 1  
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 42 cccgccgcgc gaaggcagag ccgcggacgc ccgggagcga cgagcgcgca gcgaaccggg 120  
 44 tgccgggtc atg cgc cgc cgc ctg tgg ctg ggc ctg gcc tgg ctg ctg ctg 171  
 45 Met Arg Arg Arg Leu Trp Leu Gly Leu Ala Trp Leu Leu Leu  
 46 1 5 10  
 48 gcg cgg gcg ccg gac gcc gcg gga acc ccg agc gcg tcg cgg gga ccg 219  
 49 Ala Arg Ala Pro Asp Ala Ala Gly Thr Pro Ser Ala Ser Arg Gly Pro  
 50 15 20 25 30  
 52 cgc agc tac ccg cac ctg gag ggc gac gtg cgc tgg cgg cgc ctc ttc 267  
 53 Arg Ser Tyr Pro His Leu Glu Gly Asp Val Arg Trp Arg Arg Leu Phe  
 54 35 40 45  
 56 tcc tcc act cac ttc ttc ctg cgc gtg gat ccc ggc ggc cgc gtg cag 315  
 57 Ser Ser Thr His Phe Phe Leu Arg Val Asp Pro Gly Gly Arg Val Gln  
 58 50 55 60  
 60 ggc acc cgc tgg cgc cac ggc cag gac agc atc ctg gag atc cgc tct 363  
 61 Gly Thr Arg Trp Arg His Gly Gln Asp Ser Ile Leu Glu Ile Arg Ser  
 62 65 70 75  
 64 gta cac gtg ggc gtc gtg gtc atc aaa gca gtg tcc tca ggc ttc tac 411

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Input Set : N:\Crf3\RULE60\09998966.txt

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69 Val Ala Met Asn Arg Arg Gly Arg Leu Tyr Gly Ser Arg Leu Tyr Thr
70 95                      100                      105                      110
72 gtg gac tgc agg ttc cgg gag cgc atc gaa gag aac ggc cac aac acc 507
73 Val Asp Cys Arg Phe Arg Glu Arg Ile Glu Glu Asn Gly His Asn Thr
74                      115                      120                      125
76 tac gcc tca cag cgc tgg cgc cgc cgc ggc cag ccc atg ttc ctg gcg 555
77 Tyr Ala Ser Gln Arg Trp Arg Arg Gly Gln Pro Met Phe Leu Ala
78                      130                      135                      140
80 ctg gac agg agg ggg ggg ccc cgg cca ggc ggc cgg acg cgg cgg tac 603
81 Leu Asp Arg Arg Gly Gly Pro Arg Pro Gly Gly Arg Thr Arg Arg Tyr
82                      145                      150                      155
84 cac ctg tcc gcc cac ttc ctg ccc gtc ctg gtc tcc tgaggccctg 649
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92 <211> LENGTH: 170
93 <212> TYPE: PRT
94 <213> ORGANISM: Homo sapiens
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101 20 25 30
103 Tyr Pro His Leu Glu Gly Asp Val Arg Trp Arg Arg Leu Phe Ser Ser
104 35 40 45
106 Thr His Phe Phe Leu Arg Val Asp Pro Gly Gly Arg Val Gln Gly Thr
107 50 55 60
109 Arg Trp Arg His Gly Gln Asp Ser Ile Leu Glu Ile Arg Ser Val His
110 65 70 75 80
112 Val Gly Val Val Val Ile Lys Ala Val Ser Ser Gly Phe Tyr Val Ala
113 85 90 95
115 Met Asn Arg Arg Gly Arg Leu Tyr Gly Ser Arg Leu Tyr Thr Val Asp
116 100 105 110
118 Cys Arg Phe Arg Glu Arg Ile Glu Glu Asn Gly His Asn Thr Tyr Ala
119 115 120 125
121 Ser Gln Arg Trp Arg Arg Arg Gly Gln Pro Met Phe Leu Ala Leu Asp
122 130 135 140
124 Arg Arg Gly Gly Pro Arg Pro Gly Gly Arg Thr Arg Arg Tyr His Leu
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127 Ser Ala His Phe Leu Pro Val Leu Val Ser
128 165 170
131 <210> SEQ ID NO: 3
132 <211> LENGTH: 1680
133 <212> TYPE: DNA
134 <213> ORGANISM: Homo sapiens

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/998,966

DATE: 01/29/2002

TIME: 15:45:55

Input Set : N:\Crif3\RULE60\09998966.txt

Output Set: N:\CRF3\01292002\I998966.raw

136 &lt;220&gt; FEATURE:

137 &lt;221&gt; NAME/KEY: CDS

138 &lt;222&gt; LOCATION: (177)..(1655)

140 &lt;400&gt; SEQUENCE: 3

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143 atgggctgag acacgtcctc gccgagcagt gacccttccg taccacacca gaacatgccc 120
145 gggtagacctc ctcccagatc ttccttgtag ccttcctcgc ccactccagt gacact atg 179
146                                     Met
147                                     1
149 cac ccc cac cgt gac ccg aga ggc ctc tgg ctc ctg ctg ccg tcc ttg 227
150 His Pro His Arg Asp Pro Arg Gly Leu Trp Leu Leu Leu Pro Ser Leu
151             5             10             15
153 tcc ctg ctg ctt ttt gag gtg gcc aga gct ggc cga gcc gtg gtt agc 275
154 Ser Leu Leu Leu Phe Glu Val Ala Arg Ala Gly Arg Ala Val Val Ser
155             20             25             30
157 tgt cct gcc gcc tgc ttg tgc gcc agc aac atc ctc agc tgc tcc aag 323
158 Cys Pro Ala Ala Cys Leu Cys Ala Ser Asn Ile Leu Ser Cys Ser Lys
159             35             40             45
161 cag cag ctg ccc aat gtg ccc cat tcc ttg ccc agt tac aca gca cta 371
162 Gln Gln Leu Pro Asn Val Pro His Ser Leu Pro Ser Tyr Thr Ala Leu
163 50             55             60             65
165 ctg gac ctc agt cac aac aac ctg agc cgc ctg cgg gcc gag tgg acc 419
166 Leu Asp Leu Ser His Asn Asn Leu Ser Arg Leu Arg Ala Glu Trp Thr
167             70             75             80
169 ccc acg cgc ctg acc caa ctg cac tcc ctg ctg ctg agc cac aac cac 467
170 Pro Thr Arg Leu Thr Gln Leu His Ser Leu Leu Leu Ser His Asn His
171             85             90             95
173 ctg aac ttc atc tcc tct gag gcc ttt tcc ccg gta ccc aac ctg cgc 515
174 Leu Asn Phe Ile Ser Ser Glu Ala Phe Ser Pro Val Pro Asn Leu Arg
175             100            105            110
177 tac ctg gac ctc tcc tcc aac cag ctg cgt aca ctg gat gag ttc ctg 563
178 Tyr Leu Asp Leu Ser Ser Asn Gln Leu Arg Thr Leu Asp Glu Phe Leu
179             115            120            125
181 ttc agt gac ctg caa gta ctg gag gtg ctg ctg ctc tac aat aac cac 611
182 Phe Ser Asp Leu Gln Val Leu Glu Val Leu Leu Leu Tyr Asn Asn His
183 130            135            140            145
185 atc atg gcg gtg gac cgg tgc gcc ttc gat gac atg gcc cag ctg cag 659
186 Ile Met Ala Val Asp Arg Cys Ala Phe Asp Asp Met Ala Gln Leu Gln
187             150            155            160
189 aaa ctc tac ttg agc cag aac cag atc tct cgc ttc cct ctg gaa ctg 707
190 Lys Leu Tyr Leu Ser Gln Asn Gln Ile Ser Arg Phe Pro Leu Glu Leu
191             165            170            175
193 gtc aag gaa gga gcc aag cta ccc aaa cta acg ctc ctg gat ctc tct 755
194 Val Lys Glu Gly Ala Lys Leu Pro Lys Leu Thr Leu Leu Asp Leu Ser
195             180            185            190
197 tct aac aag ctg aag aac ttg cca ttg cct gac ctg cag aag ctg ccg 803
198 Ser Asn Lys Leu Lys Asn Leu Pro Leu Pro Asp Leu Gln Lys Leu Pro
199             195            200            205
201 gcc tgg atc aag aat ggg ctg tac cta cat aac aac ccc ctg aac tgc 851

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/998,966

DATE: 01/29/2002

TIME: 15:45:55

Input Set : N:\Crf3\RULE60\09998966.txt

Output Set: N:\CRF3\01292002\I998966.raw

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205 gac tgt gag ctc tac cag ctg ttt tca cac tgg cag tat cgg cag ctg      899
206 Asp Cys Glu Leu Tyr Gln Leu Phe Ser His Trp Gln Tyr Arg Gln Leu
207                230                235                240
209 agc tcc gtg atg gac ttt caa gag gat ctg tac tgc atg aac tcc aag      947
210 Ser Ser Val Met Asp Phe Gln Glu Asp Leu Tyr Cys Met Asn Ser Lys
211                245                250                255
213 aag ctg cac aat gtc ttc aac ctg agt ttc ctc aac tgt ggc gag tac      995
214 Lys Leu His Asn Val Phe Asn Leu Ser Phe Leu Asn Cys Gly Glu Tyr
215                260                265                270
217 aag gag cgt gcc tgg gag gcc cac ctg ggt gac acc ttg atc atc aag      1043
218 Lys Glu Arg Ala Trp Glu Ala His Leu Gly Asp Thr Leu Ile Ile Lys
219                275                280                285
221 tgt gac acc aag cag caa ggg atg acc aag gtg tgg gtg aca cca agt      1091
222 Cys Asp Thr Lys Gln Gln Gly Met Thr Lys Val Trp Val Thr Pro Ser
223 290                295                300                305
225 aat gaa cgg gtg cta gat gag gtg acc aat ggc aca gtg agt gtg tct      1139
226 Asn Glu Arg Val Leu Asp Glu Val Thr Asn Gly Thr Val Ser Val Ser
227                310                315                320
229 aag gat ggc agt ctt ctt ttc cag cag gtg cag gtc gag gac ggt ggt      1187
230 Lys Asp Gly Ser Leu Leu Phe Gln Gln Val Gln Val Glu Asp Gly Gly
231                325                330                335
233 gtg tat acc tgc tat gcc atg gga gag act ttc aat gag aca ctg tct      1235
234 Val Tyr Thr Cys Tyr Ala Met Gly Glu Thr Phe Asn Glu Thr Leu Ser
235                340                345                350
237 gtg gaa ttg aaa gtg cac aat ttc acc ttg cac gga cac cat gac acc      1283
238 Val Glu Leu Lys Val His Asn Phe Thr Leu His Gly His His Asp Thr
239                355                360                365
241 ctc aac aca gcc tat acc acc cta gtg ggc tgt atc ctt agt gtg gtc      1331
242 Leu Asn Thr Ala Tyr Thr Thr Leu Val Gly Cys Ile Leu Ser Val Val
243 370                375                380                385
245 ctg gtc ctc ata tac cta tac ctc acc cct tgc cgc tgc tgg tgc cgg      1379
246 Leu Val Leu Ile Tyr Leu Tyr Leu Thr Pro Cys Arg Cys Trp Cys Arg
247                390                395                400
249 ggt gta gag aag cct tcc agc cat caa gga gac agc ctc agc tct tcc      1427
250 Gly Val Glu Lys Pro Ser Ser His Gln Gly Asp Ser Leu Ser Ser Ser
251                405                410                415
253 atg ctt agt acc aca ccc aac cat gat cct atg gct ggt ggg gac aaa      1475
254 Met Leu Ser Thr Thr Pro Asn His Asp Pro Met Ala Gly Gly Asp Lys
255                420                425                430
257 gat gat ggt ttt gac cgg cgg gtg gct ttc ctg gaa cct gct gga cct      1523
258 Asp Asp Gly Phe Asp Arg Arg Val Ala Phe Leu Glu Pro Ala Gly Pro
259                435                440                445
261 ggg cag ggt caa aac ggc aag ctc aag cca ggc aac acc ctg cca gtg      1571
262 Gly Gln Gly Gln Asn Gly Lys Leu Lys Pro Gly Asn Thr Leu Pro Val
263 450                455                460                465
265 cct gag gcc aca ggc aag ggc caa cgg agg atg tcg gat cca gaa tca      1619
266 Pro Glu Ala Thr Gly Lys Gly Gln Arg Arg Met Ser Asp Pro Glu Ser

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TIME: 15:45:55

Input Set : N:\Crf3\RULE60\09998966.txt

Output Set: N:\CRF3\01292002\I998966.raw

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267          470          475          480
269 gtc agc tcg gtc ttc tct gat acg ccc att gtg gtg tgagcaggat      1665
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271          485          490
273 ggggttggtgg ggaga      1680
276 <210> SEQ ID NO: 4
277 <211> LENGTH: 493
278 <212> TYPE: PRT
279 <213> ORGANISM: Homo sapiens
281 <400> SEQUENCE: 4
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283   1          5          10          15
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286          20          25          30
288 Ser Cys Pro Ala Ala Cys Leu Cys Ala Ser Asn Ile Leu Ser Cys Ser
289          35          40          45
291 Lys Gln Gln Leu Pro Asn Val Pro His Ser Leu Pro Ser Tyr Thr Ala
292          50          55          60
294 Leu Leu Asp Leu Ser His Asn Asn Leu Ser Arg Leu Arg Ala Glu Trp
295   65          70          75          80
297 Thr Pro Thr Arg Leu Thr Gln Leu His Ser Leu Leu Leu Ser His Asn
298          85          90          95
300 His Leu Asn Phe Ile Ser Ser Glu Ala Phe Ser Pro Val Pro Asn Leu
301          100         105         110
303 Arg Tyr Leu Asp Leu Ser Ser Asn Gln Leu Arg Thr Leu Asp Glu Phe
304          115         120         125
306 Leu Phe Ser Asp Leu Gln Val Leu Glu Val Leu Leu Tyr Asn Asn
307          130         135         140
309 His Ile Met Ala Val Asp Arg Cys Ala Phe Asp Asp Met Ala Gln Leu
310   145         150         155         160
312 Gln Lys Leu Tyr Leu Ser Gln Asn Gln Ile Ser Arg Phe Pro Leu Glu
313          165         170         175
315 Leu Val Lys Glu Gly Ala Lys Leu Pro Lys Leu Thr Leu Leu Asp Leu
316          180         185         190
318 Ser Ser Asn Lys Leu Lys Asn Leu Pro Leu Pro Asp Leu Gln Lys Leu
319          195         200         205
321 Pro Ala Trp Ile Lys Asn Gly Leu Tyr Leu His Asn Asn Pro Leu Asn
322          210         215         220
324 Cys Asp Cys Glu Leu Tyr Gln Leu Phe Ser His Trp Gln Tyr Arg Gln
325   225         230         235         240
327 Leu Ser Ser Val Met Asp Phe Gln Glu Asp Leu Tyr Cys Met Asn Ser
328          245         250         255
330 Lys Lys Leu His Asn Val Phe Asn Leu Ser Phe Leu Asn Cys Gly Glu
331          260         265         270
333 Tyr Lys Glu Arg Ala Trp Glu Ala His Leu Gly Asp Thr Leu Ile Ile
334          275         280         285
336 Lys Cys Asp Thr Lys Gln Gln Gly Met Thr Lys Val Trp Val Thr Pro
337          290         295         300
339 Ser Asn Glu Arg Val Leu Asp Glu Val Thr Asn Gly Thr Val Ser Val

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## VERIFICATION SUMMARY

DATE: 01/29/2002

PATENT APPLICATION: US/09/998,966

TIME: 15:45:56

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Output Set: N:\CRF3\01292002\I998966.raw

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L:986 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
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L:1064 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:1082 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:1159 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:1160 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:1183 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:1184 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:1356 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14  
L:1374 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14  
L:1996 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (25) SEQUENCE: